

=> d his

(FILE 'HOME' ENTERED AT 12:35:06 ON 20 NOV 2007)

FILE 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ESBIODASE, FOMAD, ...' ENTERED AT 12:35:22 ON 20 NOV 2007

L1	506 S ADENOVIRUS AND SHAFT AND KNOB AND (MODIFICATION OR MUTATION)
L2	62 S L1 AND ((AB OR CD) (S) LOOP)
L3	14 S L2 AND (K01 OR K01)
L4	8 DUP REMOVE L3 (6 DUPLICATES REMOVED)
L5	1 S NEMEROW G/AU AND (AB (S) LOOP)

SCORE Search Results Details for Application 10560250 and Search Result 20071114_085436_us-10-560-250-48.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10560250 and Search Result 20071114_085436_us-10-560-250-48.rag.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 14, 2007, 08:54:49 ; Search time 269 Seconds
(without alignments)
29.105 Million cell updates/sec

Title: US-10-560-250-48
Perfect score: 82
Sequence: 1 IGINVRAREGLTFDND 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	16	9	ADW21172	Adw21172 Human ade
2	82	100.0	365	4	AAG62575	Aag62575 Follicula
3	82	100.0	365	4	AAG62574	Aag62574 Follicula
4	82	100.0	365	8	ADU77462	Adu77462 Adenoviru
5	82	100.0	365	8	ADU77464	Adu77464 Adenoviru
6	82	100.0	365	9	ADW21164	Adw21164 Human ade
7	82	100.0	365	9	ADW21162	Adw21162 Human ade
8	82	100.0	365	9	AEB96796	Aeb96796 Adenoviru
9	82	100.0	365	9	AEB96790	Aeb96790 Adenoviru
10	82	100.0	365	10	AEJ26288	Aej26288 Adenoviru
11	82	100.0	366	9	ADW21181	Adw21181 Chimeric
12	82	100.0	380	3	AAY68659	Aay68659 Amino aci
13	82	100.0	380	4	AAB67187	Aab67187 Mastadeno
14	82	100.0	380	4	AAB31744	Aab31744 Amino aci
15	82	100.0	578	9	ADW21179	Adw21179 Chimeric
16	77	93.9	366	4	AAG62573	Aag62573 Follicula
17	77	93.9	366	6	AAO26480	Aao26480 Adenoviru
18	77	93.9	366	6	AAO30863	Aao30863 Adenoviru
19	77	93.9	366	9	AEB96788	Aeb96788 Adenoviru
20	70	85.4	335	3	AAY68650	Aay68650 Amino aci
21	70	85.4	335	4	AAB67178	Aab67178 Mastadeno
22	70	85.4	335	4	AAB31735	Aab31735 Amino aci
23	47	57.3	559	6	AAO23319	Aao23319 Rhesus mo
24	43	52.4	124	7	AEJ43914	Aej43914 A. actino
25	43	52.4	124	8	ADO57560	Ado57560 Actinobac
26	43	52.4	124	10	AEJ26895	Aej26895 A. actino
27	43	52.4	340	3	AAY68666	Aay68666 Amino aci
28	43	52.4	340	4	AAB67194	Aab67194 Mastadeno
29	43	52.4	340	4	AAB31751	Aab31751 Amino aci
30	42	51.2	211	6	ABU45325	Abu45325 Protein e
31	42	51.2	211	6	ABU47972	Abu47972 Protein e
32	42	51.2	436	4	AAB59872	Aab59872 Carbon mo
33	42	51.2	481	6	ABM69091	Abm69091 Photorhab
34	41	50.0	71	4	AAU60485	Aau60485 Propionib
35	41	50.0	71	6	ABM57004	Abm57004 Propionib
36	41	50.0	111	6	ABM64747	Abm64747 Propionib
37	41	50.0	662	4	AAE00939	Aae00939 Human 15S
38	41	50.0	662	7	ADD47873	Add47873 Human Pro
39	41	50.0	662	8	ADJ75368	Adj75368 Marker ge
40	41	50.0	662	8	ADQ91786	Adq91786 Human 15S
41	41	50.0	662	8	ADQ37894	Adq37894 Human 15-
42	41	50.0	684	5	ABB08005	Abb08005 Human lip
43	40	48.8	194	6	ABU31822	Abu31822 Protein e
44	40	48.8	241	9	ABM91696	Abm91696 M. xanthu
45	40	48.8	247	7	ABO61404	Abo61404 Klebsiell

ALIGNMENTS

RESULT 1

ADW21172

ID ADW21172 standard; peptide; 16 AA.

XX

AC ADW21172;

<!--StartFragment-->RESULT 12

AA68659

ID AAY68659 standard; protein; 380 AA.

XX

AC AAY68659;

XX

DT 12-SEP-2003 (revised)

DT 05-MAY-2000 (first entry)

XX

DE Amino acid sequence of the fiber protein of Adenovirus serotype 37.

XX

KW Chimaeric adenovirus; gene therapy; antigenicity; fiber protein;

KW serotype 37; penton protein; hexon protein.

XX

OS unidentified adenovirus.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .29

FT /note= "part of the tail of adenovirus serotype 5"

XX

PN WO200003029-A2.

XX

PD 20-JAN-2000.

XX

PF 08-JUL-1999; 99WO-NL000436.

XX

PR 08-JUL-1998; 98EP-00202297.

XX

PA (INTR-) INTROGENE BV.

XX

PI Havenga M, Vogels R, Bout A;

XX

DR WPI; 2000-171149/15.

XX

PT New chimaeric adenoviruses containing a genome derived from different

PT adenovirus serotypes, useful in gene therapy.

XX

PS Example 2; Fig 7; 92pp; English.

XX

CC AAY68642-70 represent the amino acid sequences of the fiber proteins of
 CC Adenovirus serotypes 8, 9, 13, 14, 20, 23, 24, 25, 27, 28, 29, 30, 32,
 CC 33, 34, 35, 36, 37, 38, 39, 42, 43, 44, 45, 46, 47, 48, 49 and 51. The
 CC proteins are used in the course of the invention to construct chimaeric
 CC adenoviruses with reduced antigenicity. The chimaeric adenoviruses
 CC comprise at least part of a fiber protein of an adenovirus serotype
 CC providing the chimaeric virus with a desired host range and at least part
 CC of a penton or hexon protein from another, less antigenic, serotype. The
 CC chimaeric adenoviruses are useful for gene therapy, especially where
 CC repeated delivery is required. Adenoviruses of the invention are useful
 CC can be constructed to have a desired host range and a diminished
 CC capability to raise neutralizing antibodies, an absence of, or decreased
 CC infection of, antigen presenting cells of the immune system (e.g.
 CC macrophages), and an ability to escape trapping in the liver through
 CC increased target cell specificity. (Updated on 12-SEP-2003 to standardise
 CC OS field)

XX

SQ Sequence 380 AA;

Query Match 100.0%; Score 82; DB 3; Length 380;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IGINVRAREGLTFDND 16
|||||||
Db 171 IGINVRAREGLTFDND 186

RESULT 13
<!--EndFragment-->

```
<!--StartFragment-->RESULT 6
US-09-348-354A-31
; Sequence 31, Application US/09348354A
; Publication No. US20030017138A1
; GENERAL INFORMATION:
; APPLICANT: Havenga, Menzo
; APPLICANT: Vogels, Ronald
; APPLICANT: Bout, Abraham
; TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
; FILE REFERENCE: 2183-4123US
; CURRENT APPLICATION NUMBER: US/09/348,354A
; CURRENT FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Human Adenovirus 37 Fiber Protein
US-09-348-354A-31
```

```
Query Match          100.0%; Score 82; DB 3; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy          1 IGINVRAREGLTFDND 16
             |||||
Db          170 IGINVRAREGLTFDND 185
<!--EndFragment-->
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